CASSAVA MOSAIC DISEASE IN MADAGASCAR: COMPLEX EPIDEMIOLOGY AND EVOLUTIONARY DYNAMICS OF CASSAVA MOSAIC GEMINIVIRUSES

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BACKGROUND and OBJECTIVES

Cassava is the staple food for hundreds of millions of people in Africa but its cultivation is seriously constrained by cassava mosaic disease (CMD) in Madagascar and in Africa in general. We have undertaken (1) to identify the cassava mosaic geminiviruses (CMGs) involved in CMD in Madagascar and their epidemiological characteristics from country-wide surveys, and (2) to study the genetic and spatial structure of Malagasy CMGs populations.

MATERIAL and METHODS

Altogether 708 cassava leaf samples were collected with and without CMD symptoms from the main cassava-growing areas of Madagascar during 2009 to 2011. Prevalence and symptom severity of CMD, origin of infection (whitefly or cutting), and abundance of whiteflies were assessed.

RESULTS

Molecular diagnosis of CMGs in Madagascar revealed an unprecedented diversity and co-occurrence of six CMGs. Distinct geographical distributions were observed for the six viruses. While EACMCV and SACMV were widespread, ACMV was more prevalent in the central highlands, and EACMV and EACMKV were prevalent in lowlands and coastal regions. PCR diagnosis revealed that mixed infection (up to four co-infected viruses) occurred in 21% of the samples and were associated with higher symptom severity scores. Pairwise comparisons of virus associations showed that EACMCV was found in mixed infections more often than expected while ACMV and SACMV were mostly found in single infections. Even if the whitefly vector *Bemisia tabaci* was more abundant in lowland and coastal areas, infected cuttings remain the primary source of CMD propagation (95%) in Madagascar.
SACMV and ACMV, the two most prevalent viruses, displayed low degrees of genetic diversity and have most likely been introduced to the island only once. By contrast, EACMV-like CMG populations (EACMV, EAMCKV, EACMCV and complex recombinants of these) were more diverse, more spatially structured, and displayed evidence of at least three independent introductions from mainland Africa.

CONCLUSIONS

Our study highlights both the complexity of CMD in Madagascar, and the distinct evolutionary and spatial dynamics of the different viral species that collectively are associated with this disease.

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